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16

RAW SEQUENCE LISTING

DATE: 11/13/2003

PATENT APPLICATION: US/09/862,802A

TIME: 15:55:57

Input Set : A:\SF0695BUS.ST25.txt

Output Set: N:\CRF4\11132003\I862802A.raw

3 <110> APPLICANT: Valladeau, Jenny
4 Ravel, Odile
5 Bates, Elizabeth Ester Mary
6 Ford, John
7 Lebecque, Serge J.E.
8 Saeland, Sem
10 <120> TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
12 <130> FILE REFERENCE: SF0695 B
14 <140> CURRENT APPLICATION NUMBER: US 09/862,802A
15 <141> CURRENT FILING DATE: 2001-05-22
17 <150> PRIOR APPLICATION NUMBER: US 60/053,080
18 <151> PRIOR FILING DATE: 1997-07-09
20 <150> PRIOR APPLICATION NUMBER: US 09/111,470
21 <151> PRIOR FILING DATE: 1998-07-08
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1104
29 <212> TYPE: DNA
30 <213> ORGANISM: Unknown
32 <220> FEATURE:
33 <223> OTHER INFORMATION: mammalian nucleic acid and protein
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (242)..(952)
38 <223> OTHER INFORMATION:

ENTERED

> 41 <400> 1

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44 gtggttctta gttctcatga gaccctctt gaggatatgt gcctatctgg tgcctctgct      120
46 ctccactagt tgagtgaag gaaggaggta atttaccacc atgtttgggt cctgtttata      180
48 agatgtttta agaaagattt gaaacagatt ttctgaagaa agcagaagct ctcttcccat      240
50 t atg act tcg gaa atc act tat gct gaa gtg agg ttc aaa aat gaa ttc      289
51 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
52 1          5          10          15
54 aag tcc tca ggc atc aac aca gcc tct tct gca gct tcc aag gag agg      337
55 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
56          20          25          30
58 act gcc cct ctc aaa agt aat acc gga ttc ccc aag ctg ctt tgt gcc      385
59 Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
60          35          40          45
62 tca ctg ttg ata ttt ttc ctg cta ttg gca atc tca ttc ttt att gct      433
63 Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
64          50          55          60

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66 ttt gtc att ttc ttt caa aaa tat tct cag ctt ctt gaa aaa aag act      481
67 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
68 65                               70                               75                               80
70 aca aaa gag ctg gtt cat aca aca ttg gag tgt gtg aaa aaa aat atg      529
71 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
72                               85                               90                               95
74 ccc gtg gaa gag aca gcc tgg agc tgt tgc cca aag aat tgg aag tca      577
75 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
76                               100                              105                              110
78 ttt agt tcc aac tgc tac ttt att tct act gaa tca gca tct tgg caa      625
79 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
80                               115                              120                              125
82 gac agt gag aag gac tgt gct aga atg gag gct cac ctg ctg gtg ata      673
83 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
84                               130                              135                              140
86 aac act caa gaa gag cag gat ttc atc ttc cag aat ctg caa gaa gaa      721
87 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
88 145                               150                              155                              160
90 tct gct tat ttt gtg ggg ctc tca gat cca gaa ggt cag cga cat tgg      769
91 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
92                               165                              170                              175
94 caa tgg gtt gat cag aca cca tac aat gaa agt tcc aca ttc tgg cat      817
95 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
96                               180                              185                              190
98 cca cgt gag ccc agt gat ccc aat gag cgc tgc gtt gtg cta aat ttt      865
99 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
100                               195                              200                              205
102 cgt aaa tca ccc aaa aga tgg ggc tgg aat gat gtt aat tgt ctt ggt      913
103 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
104                               210                              215                              220
106 cct caa agg tca gtt tgt gag atg atg aag atc cac tta tgaactgaac      962
107 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
108 225                               230                              235
110 attctccatg aacaggtggt tggattggta tctgtcattg tagggataga taataagctc 1022
112 ttcttattca tgtgtaaggg aggtccatag aatttaggtg gtctgtcaac tattctactt 1082
114 atgagagaat tggctctgtac at                                           1104
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 237
119 <212> TYPE: PRT
120 <213> ORGANISM: Unknown
122 <220> FEATURE:
123 <223> OTHER INFORMATION: mammalian nucleic acid and protein
125 <400> SEQUENCE: 2
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128 1                               5                               10                               15
131 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
132                               20                               25                               30
135 Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
136                               35                               40                               45

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139 Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
140      50      55      60
143 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Glu Lys Lys Thr
144 65      70      75      80
147 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
148      85      90      95
151 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
152      100      105      110
155 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
156      115      120      125
159 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
160      130      135      140
163 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
164 145      150      155      160
167 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
168      165      170      175
171 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
172      180      185      190
175 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
176      195      200      205
179 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
180      210      215      220
183 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
184 225      230      235

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187 <210> SEQ ID NO: 3

188 <211> LENGTH: 1458

189 <212> TYPE: DNA

190 <213> ORGANISM: Unknown

192 <220> FEATURE:

193 <223> OTHER INFORMATION: mammalian nucleic acid and protein

195 <220> FEATURE:

196 <221> NAME/KEY: CDS

197 <222> LOCATION: (257)..(1204)

198 <223> OTHER INFORMATION: protein coding sequence

201 <220> FEATURE:

202 <221> NAME/KEY: misc_feature

203 <222> LOCATION: (608)..(673)

204 <223> OTHER INFORMATION: short form lacks nucleotides 608-673

207 <220> FEATURE:

208 <221> NAME/KEY: misc_feature

209 <222> LOCATION: (775)..(776)

210 <223> OTHER INFORMATION: ASGPRm (Table 2) has sequence insert encoding GEE between nucleotides 775-776

214 <220> FEATURE:

215 <221> NAME/KEY: misc_feature

216 <222> LOCATION: (1064)..(1064)

217 <223> OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather than Asp at the residue numbered 270

221 <400> SEQUENCE: 3

RAW SEQUENCE LISTING

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Input Set : A:\SF0695BUS.ST25.txt

Output Set: N:\CRF4\11132003\I862802A.raw

222	gttgaggaga	tgggatgtcc	cagatgatag	ggctcctggg	atttcagacc	caagaccagc	60	
224	aggactccag	tcacctctac	cccagctctc	caggacacag	cgctcccaac	tctgagtgc	120	
226	gtcccacctc	tggtccttgc	agcacaacca	acgtgggaat	cacacctcc	agacctccca	180	
228	cagctccacc	ccagactggg	cgccggccct	gcctccattt	cagctgtgac	aacctcagag	240	
230	ccgtgttggc	ccaagc atg	aca agg acg	tat gaa aac	ttc cag tac	ttg gag	292	
231		Met Thr Arg	Thr Tyr Glu	Asn Phe	Gln Tyr	Leu Glu		
232		1	5	10				
234	aat aag	gtg aaa	gtc cag	ggg ttt	aaa aat	ggg cca	ctt cct ctc cag	340
235	Asn Lys	Val Lys	Val Gln	Gly Phe	Lys Asn	Gly Pro	Leu Pro Leu Gln	
236		15	20	25				
238	tcc ctc	ctg cag	cgt ctc	cgc tct	ggg ccc	tgc cat	ctc ctg ctg tcc	388
239	Ser Leu	Leu Gln	Arg Leu	Arg Ser	Gly Pro	Cys His	Leu Leu Leu Ser	
240		30	35	40				
242	ctg ggc	ctc ggc	ctg ctg	ctg ctg	gtc atc	atc tgt	gtg gtt gga ttc	436
243	Leu Gly	Leu Gly	Leu Leu	Leu Leu	Val Ile	Ile Cys	Val Val Gly Phe	
244	45	50	55	60				
246	caa aat	tcc aaa	ttt cag	agg gac	ctg gtg	acc ctg	aga aca gat ttt	484
247	Gln Asn	Ser Lys	Phe Gln	Arg Asp	Leu Val	Thr Leu	Arg Thr Asp Phe	
248		65	70	75				
250	agc aac	ttc acc	tca aac	act gtg	gcg gag	atc cag	gca ctg act tcc	532
251	Ser Asn	Phe Thr	Ser Asn	Thr Val	Ala Glu	Ile Gln	Ala Leu Thr Ser	
252		80	85	90				
254	cag ggc	agc agc	ttg gaa	gaa acg	ata gca	tct ctg	aaa gct gag gtg	580
255	Gln Gly	Ser Ser	Leu Glu	Glu Thr	Ile Ala	Ser Leu	Lys Ala Glu Val	
256		95	100	105				
258	gag ggt	ttc aag	cag gaa	cgg cag	gca ggg	gta tct	gag ctc cag gaa	628
259	Glu Gly	Phe Lys	Gln Glu	Arg Gln	Ala Gly	Val Ser	Glu Leu Gln Glu	
260		110	115	120				
262	cac act	acg cag	aag gca	cac cta	ggc cac	tgt ccc	cac tgc cca tct	676
263	His Thr	Thr Gln	Lys Ala	His Leu	Gly His	Cys Pro	His Cys Pro Ser	
264	125	130	135	140				
266	gtg tgt	gtc cca	gtt cat	tct gaa	atg ctc	ctg cga	gtc cag cag ctg	724
267	Val Cys	Val Pro	Val His	Ser Glu	Met Leu	Leu Arg	Val Gln Gln Leu	
268		145	150	155				
270	gtg caa	gac ctg	aag aaa	ctg acc	tgc cag	gtg gct	act ctc aac aac	772
271	Val Gln	Asp Leu	Lys Lys	Leu Thr	Cys Gln	Val Ala	Thr Leu Asn Asn	
272		160	165	170				
274	aat gcc	tcc act	gaa ggg	acc tgc	tgc ccc	gtc aac	tgg gtg gag cac	820
275	Asn Ala	Ser Thr	Glu Gly	Thr Cys	Cys Pro	Val Asn	Trp Val Glu His	
276		175	180	185				
278	caa gac	agc tgc	tac tgg	ttc tct	cac tct	ggg atg	tcc tgg gcc gag	868
279	Gln Asp	Ser Cys	Tyr Trp	Phe Ser	His Ser	Gly Met	Ser Trp Ala Glu	
280		190	195	200				
282	gct gag	aag tac	tgc cag	ctg aag	aac gcc	cac ctg	gtg gtc atc aac	916
283	Ala Glu	Lys Tyr	Cys Gln	Leu Lys	Asn Ala	His Leu	Val Val Ile Asn	
284	205	210	215	220				
286	tcc agg	gag gag	cag aat	ttt gtc	cag aaa	tat cta	ggc tcc gca tac	964
287	Ser Arg	Glu Glu	Gln Asn	Phe Val	Gln Lys	Tyr Leu	Gly Ser Ala Tyr	
288		225	230	235				

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290 acc tgg atg ggc ctc agt gac cct gaa gga gcc tgg aag tgg gtg gat      1012
291 Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp
292          240          245          250
294 gga aca gac tat gcg acc ggc ttc cag aac tgg aag cca ggc cag cca      1060
295 Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro
296          255          260          265
298 gac gac tgg cag ggg cac ggg ctg ggt gga ggc gag gac tgt gct cac      1108
299 Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala His
300          270          275          280
302 ttc cat cca gac ggc agg tgg aat gac gac gtc tgc cag agg ccc tac      1156
303 Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr
304 285          290          295          300
306 cac tgg gtc tgc gag gct ggc ctg ggt cag acc agc cag gag agt cac      1204
307 His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
308          305          310          315
310 tgagctgcct ttggtgggac caccggcca cagaaatggc ggtgggagga ggactcttct      1264
312 cagcactcc tcgcaagacc gctctgggag agaaataagc actgggagat tggaagcact      1324
314 gctaacattt tgaatttttt tctctttaat tttaaaaaga tggatatagt ttcttaagct      1384
316 tttatttttt ttccaacttt tgaaagtcaa cttcatgaag gtataatttt tacataataa      1444
318 aaatgcactc attt      1458
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 316
323 <212> TYPE: PRT
324 <213> ORGANISM: Unknown
326 <220> FEATURE:
327 <223> OTHER INFORMATION: mammalian nucleic acid and protein
329 <220> FEATURE:
330 <221> NAME/KEY: misc_feature
331 <222> LOCATION: (608)..(673)
332 <223> OTHER INFORMATION: short form lacks nucleotides 608-673
334 <220> FEATURE:
335 <221> NAME/KEY: misc_feature
336 <222> LOCATION: (775)..(776)
337 <223> OTHER INFORMATION: ASGPRm (Table 2) has sequence insert encoding GEE between nucleot
338      ides 775-776
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (1064)..(1064)
343 <223> OTHER INFORMATION: nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
344      than Asp at the residue numbered 270
346 <400> SEQUENCE: 4
348 Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
349 1          5          10          15
352 Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
353          20          25          30
356 Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
357          35          40          45
360 Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
361          50          55          60

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VERIFICATION SUMMARY

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Input Set : A:\SF0695BUS.ST25.txt

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1 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:38